

Exhibit A

BLAST 2 SEQUENCES alignment of SEQ ID NO: 3 with 12ge20305orf30, a hypothetical *H. pylori* ORF disclosed by Smith et al. in WO 96/40893.



Blast 2 Sequences results

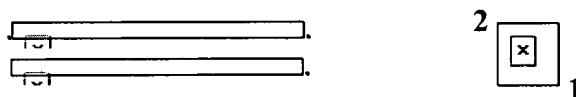
[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 Length 759 (1 .. 759)

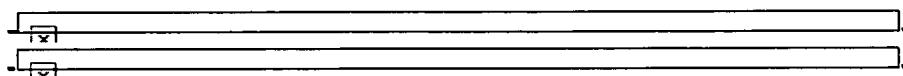
Sequence 2 lcl|seq_2 Length 768 (1 .. 768)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1344 bits (699), Expect = 0.0
Identities = 737/756 (97%)
Strand = Plus / Plus



Query: 1 atggcatacaaatatgatagagacttggaaatttttaaaggcaatttggaaatcttagtgattta
60
Sbjct: 10 atggcatacaaatatgatagagacttggaaatttttaaaggcaacttggaaatcttagtgattta
69

Query: 61 ttggatttgttgagggtgcttgtttggtaaaggacggcgaaaaaaaagacacaatgaaaaaa
120
Sbjct: 70 ttggatttgttcgagggtgcttgtttggtaaaggacggcgaaaaaaaagacacaatgaaaaaa
129

Query: 121 ctgaccagctccatagaatacacaaaaaggcatggcgatgattacgctaaatacgcagaaaga
180 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 130 ctcacaagctccatagaatacacaaaaaggcatggcgatgattacgctaaatacgcagaaaga
189 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 181 atcgctgaagagttgcaataactatggagcaatagtttgcagttcattaaaggcgaa
240 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 190 atcgctgaagagttgcaataactatggagcaatagtttgcagttcattaaagggtgaa
249 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 241 ggagtcttatacaaagagatttatgcgtgtgcgataaattaaaggtaattacaac
300 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 250 ggagtcttatacaaagagatttatgcgtgtgcgataaattaaaggtaattacaac
309 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 301 aagaaaactgaaacgacttaattgaacaaaacatgcttctaaaatcttagaaagaagt
360 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 310 aagaaaactgaaacgacttaattgaacaaaacatgcttctaaaatcttagaaagaagc
369 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 361 ttggaagaaatggatgatgaagaagtgaaagaaatgtgcgtatgaattatccataaaaaac
420 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 370 ctagaagaaatggatgatgaagaagtgaaagaaatgtgcgtatgaattgtccataaaaaac
429 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 421 acggacaatttaaacagacaagccttaagcgccggcgactttAACGCTGTAAATGGGG
480 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 430 acggacaatttgaacagacaagccttaagcgccggcgactttAACGCTGTAAATGGGA
489 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 481 ggTTTAAATCTTATCAATTAGCTGTCAATTGCGAATGCCTGCGAAACCCATTCTA
540 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 490 ggCTTAAATCTTATCAATTAGCTGTCAATTGCGAATGCCTGCGAAACCCATTCTA
549 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 541 gggcgtggTTATCGCTTGCgggcaatcaggtgcttacaagaactctgagcttttaaca
600 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 550 gggcgtggTTATCGCTTGCgggcaatcagtgcttacaagaactctgagcttttaaca
609 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 601 ggtcctgttggctggatcattacaggcgtatggacagcgattgatattgcagggccggct
660 || || || || || || || || || || || || || || || || || || || || || || || || ||
Sbjct: 610 ggccctgttggctggatcattacaggcgtatggacagcgattgatattgcagggccggct
669

Query: 661 tataggtaaccataccggcatgcattgtggccactttacgcctaaaaacacagcaa
720 || || || || || || || || || || || || || || || || || || || || || || || || || || || || ||
Sbjct: 670 tataggtaaccataccggcatgcattgtggccactttacgcctaaaaacgcacaa
729

Query: 721 gccaatggagataagaagtgcgttgc当地atcc 756
|| || || || || || || || || || || || || || || || || || || || || || || || || || || || || ||
Sbjct: 730 gccaatgaagataagaagtgcgttgc当地atcc 765

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total
secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 166
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 759
Length of database: 12,305,973,192
Length adjustment: 26
Effective length of query: 733
Effective length of database: 12,305,973,166
Effective search space: 9020278330678
Effective search space used: 9020278330678
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)

CODING SEQUENCE WITH HOMOLOGY TO SEQ ID NO: 3 DISCLOSED BY
SMITH ET AL.

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 186778-60-9 REGISTRY
CN DNA (*Helicobacter pylori* strain J99 open reading frame
12ge20305orf30)
 (9CI) (CA INDEX NAME)
FS NUCLEIC ACID SEQUENCE
SQL 768
NA 268 a 123 c 178 g 199 t
NTE doublestranded

SEQ 1 aggaataata tggcatacaa atatgataga gacttggaaat ttttaagca
 51 actggaatct agtgattttt tggatttgtt cgaggtgctt gtttttggta
 101 aagacggcga aaaaagacac aatgaaaaaac tcacaagctc catagaatac
 151 aaaaggcatg gcgatgatta cgctaaatac gcagaaagaa tcgctgaaga
 201 gttgcaatac tatgggagca atagtttgc gagtttcatt aaaggtgaag
 251 gagtcctata caaagagatt ttatgcgatg tgtgcgataa attaaaggc
 301 aattacaaca agaaaaactga aacgacttta attgaacaaa acatgcttc
 351 taaaatctta gaaagaagcc tagaagaaat ggatgatgaa gaagtgaaag
 401 aaatgtgcga tgaattgtcc ataaaaaaaaaca cggacaattt gaacagacaa
 451 gccttaagcg cggcgacttt aacgctgttt aaaatgggag gctttaaatc
 501 ttatcaatta gctgtcattt tgcaatgc ggttgcaaaa accattctag
 551 ggcgtggttt atcgcttgcg ggcaatcaag tgcttacaag aactctgagc
 601 ttttaacag gccctgtgg ctggatcatt acaggcgtat ggacagcgtat
 651 tgatattgca gggccggctt ataggtaac cataccggca tgcattgtgg
 701 tcgccacttt acgcctaaaa acgcaacaag ccaatgaaga taagaagtgc
 751 ttgcaaatacg aatccgtt

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL
DT.CA CAplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

HP30 Coding Sequence, SEQ ID NO: 3

atggcatacaaatatgatagagacttggaatTTTaaAGcaattggaatcttagtgattta
ttggatttgggttgtttggtaaAGacggcgaaaaAGacacaatggaaaa
ctgaccagctccatagaatacAAAAGGcatggcgatgattacgctaaatacgcagaaaga
atcgctgaagagtgcataactatggagcaatagtttgcgagttcattaaaggcgaa
ggagtcttatacaaAGAGATTtatgcgtgtgcgataAAAGGTcaattacaac
aagaaaactgaaACGactttaattgaacAAAACATgcttcattaaatcttagaaAGt
ttggaaAGAAATGGatgatgaaAGtggaaAGAATgtgcgatgattatccataaaaaac
acggacaatttaaacagacaAGCCTtaagcgcggcgactttAACGCTGTTAAATGGGG
ggTTTAAATCTTatcaatttagctgtcattgtgcgatgcggcgcggcaaaaaaccattcta
ggcgtggTTatcgcttgcggcaatcaggcgatggacagcgcattgtgcggccactttacgcctaaaaacacagcaa
gttcctgtggcgtggatcattacaggcgatggacagcgcattgtggccactttacgcctaaaaacacagcaa
tataggtaaccataccggcatgcattgtggccactttacgcctaaaaacacagcaa
gccaatggagataagaAGTCGTTGCAAATAGATCCATT